

31208047.i10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150.....160.....170.....180.....190.....20.....
24648121.f MSLNQHSGPGPSEICGLSVQDSSAASPFIVSTAGMCTTATTVTTSTNGDATAEAPVKHQFLHNGWIGNGLPPAVPRTISSDRLVTSSCRARTSAWSRDTNLK
31981902.m MDRSKRNSIAGFIPR-VERLEDFEGGGGCDNTYQVGRVSSSPLAISASRPTSLDDFTPR EKIGSCFFSVYKVRHRTQVMVRLRANRNM
19173754.m MDRSKRNSIAGFIPR-VERLEDFEGGGGCDNTYQVGRVSSSPLAISASRPTSLDDFTPR EKIGSCFFSEVFKVRHRASQCVMLKMLNLSNRNL
TESK2.h MDRSKRNSIAGFIPR-VERLEDFEGGGGCDNTYQVGRVSSSPLAISASRPTSLDDFTPR EKIGSCFFSEVFKVRHRASQCVMLKMLNLSNRNL
31543857.m MAG-ERPPRGCPGP-BAPCEGP-CGAGG-GPGRGR-SRRAISARSAWSRDTNLKDDCATEKIGCAFFSEVYKVRHRASQCVMLKMLNLSNRNL
13928784.m MAG-ERPPRGCPGP-BAPCEGP-CGAGG-GPGRGR-SRRAISARSAWSRDTNLKDDCATEKIGCAFFSEVYKVRHRASQCVMLKMLNLSNRNL
TESK1.h MAG-ERPPRGCPGP-BAPCEGP-CGAGG-GPGRGR-SRRAISARSAWSRDTNLKDDCATEKIGCAFFSEVYKVRHRASQCVMLKMLNLSNRNL
34862016.m MAALARALVELDRNVNPDVGQAP-SNGANCPLPENTGRAKINGFCKKLICSAISOKAISPAFTGLOPFSRTRTLCGECNDLGRIVWGFQRTKRR-RPACALISDSCR-
SgK493.h MRRRAAAVAEFCASFLLGSVLNVLFAFPGSEPPS1APGPGRGGRRGEARQIRARYDEVORYSRGEGPGCAGRPERRRLMDAPGPP-LPFWAR-
lias_TGFBR EDPSLDLDPFISEGTTIKCIIYMTTSGCSPFLLVEITIAR-TIVLCEPKKPFSEVTPK-N-CEPVAVKTFSSREBFWFREBLYQTIVWLRBENILICFTADNKDNGTWTDWLVSDPHGCFDDE

210.....220.....230.....240.....250.....260.....270.....280.....290.....300.....310.....320.....330.....340.....350.....360.....370.....380.....390.....40.....
31208047.i ANKAQYDPAWLKIRIALGIAARGQYVHDYIFIFRDLTSK-
24648121.f ANKEAVVLSATKPLAALGIAARGQYVHDYIFIFRDLTSK-
31981902.m D-SDLYPWTWVRLVLAIDIAVGSYVHLKRCIFHRDLTSKNCNLLKR-
19173754.m D-SNLQYWTWVRLVLAIDIAVGSYVHLKRCIFHRDLTSKNCNLLKR-
TESK2.h D-SNLBWTWVRLVLAIDIAVGSYVHLKRCIFHRDLTSKNCNLLKR-
31543857.m S-SPEPISWPVRLLAIDIAQGKRYLIAHKGVIFHRDLTSKNCNLLKR-
13928784.m S-SPEPISWPVRLLAIDIAQGKRYLIAHKGVIFHRDLTSKNCNLLKR-
TESK1.h S-SPEPISWPVRLLAIDIAQGKRYLIAHKGVIFHRDLTSKNCNLLKR-
34862016.m S-GYTKAVYRVLRLPCCGAAVAKADFCSHDLGSCVRFVYRRG-
SgK493.h S-GYTKAVYRVLRLPCCGAAVAKADFCSHDLGSCVRFVYRRG-
lias_TGFBR N-RTYVTEGMKMLALSTASCPAHLHMP2VGT

410.....420.....430.....440.....450.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....60.....
31208047.i GSATSGVGN-GLNSTSSSEPVFAVESENVSAGSS-TTTPSSSEGEYSNPPLHRRSLSENVIVEPP-
24648121.f GGSDENVNTLPRASVPTVATICATAPAGLTLTPRHLQEVDGFRFPSSKKSASAALPGTPNGSAGSSGFDHILKSRVRRATQKLEAIIHLRRSLSENIHPPMITS-
31981902.m VPGKKRLLSDD-D-
19173754.m VPGKKRLLSDD-D-
TESK2.h APGVKRLSDD-D-
31543857.m NQGSVPVRGGPS-
13928784.m NQGSVPVRGGPS-
TESK1.h ATLPRPDR-
34862016.m ATLPRPDR-
SgK493.h ATLPRPDR-
lias_TGFBR SPENWGDNLYLTVNPFSREDLROGKHLKD

610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750.....760.....770.....780.....790.....80.....
31208047.i PKAVTYYSGDIFSSCPEIASPYFRAWNSVQNOIVRNAREGRSCAGGMANS-
24648121.f NPKTYAAGCGLFSSCFEMIAPPFKKELAAMQSCKAG-AQGGGTTSTEETSGNKAASATPSE-PKSILPVSPHMTRNYSAILRLPQRISNAAPPV-
31981902.m LPSKSVISLVLFDL-
19173754.m LPSKSVISLVLFDL-
TESK2.h LPSKSVISLVLFDL-
31543857.m TPCKPATPLPVLPP-
13928784.m TPCKPATPLPVLPP-
TESK1.h TPSK-
34862016.m YNAKRFFFYTILP-
SgK493.h YNAKRFFFYTILP-
lias_TGFBR IHEDYQLPYYDLP-

810.....820.....830.....840.....850.....860.....870.....880.....890.....900.....910.....920.....930.....940.....950.....960.....970.....980.....990.....100.....
31208047.i EVASAGATAAAKSSTATGTSSAASPNVNLSTVKMNGSVK-PIMPSIVSEDVDEELE-LNEEE-
24648121.f VGATNSCDELTEGARKSKEQASSGATAAVQALTPMSGCSTRLVETPVSVSSCTDLELDLKNTCDLNELKN-
31981902.m ACPPFC-CEPSSLSD-
19173754.m ACPPFC-CEPSSLSD-
TESK2.h ACPPFC-CEPSSLSD-
31543857.m ETALCPGPSPMGP-TEERMDCCECSPE-
13928784.m ETALCPGPSPVGPSTEEAMDCECSPE-
TESK1.h ETALCPGPAPAVGSPAAEKCMCECSPE-
34862016.m DSTITQEDYRCWPSYHHGCLLSVNLNEAVDVCESHSYCRAFVTNTQTT-
SgK493.h DSTIPQDYRCWPSYHHGCLLSVNLNEAVDVCESHSYCRAFVTNTQTT-
lias_TGFBR AARLTALRIKTKLISOLSQEQEJKM

1010.....1020.....1030.....1040.....1050.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....120.....
31208047.i
24648121.f SSILVFDSSSTVSSLRSMDLADLSDSIRKRFNHLLIPVHHQHNRHLLSNVDPDARSITDMG-
31981902.m DCNPQEE-NFGPRLKGTSCTGAASEEEVEE-
19173754.m DCNPQEE-NFGPRLKGTSCTGAASEEEVEE-
TESK2.h DCNPQEE-NFGPRLKGTSCTGAASEEEVEE-
31543857.m ETALCPGPSPMGP-TEERMDCCECSPE-
13928784.m ETALCPGPSPVGPSTEEAMDCECSPE-
TESK1.h ETALCPGPAPAVGSPAAEKCMCECSPE-
34862016.m ETLAQEMVHLFRSGQYLNQTSR-AEYORIP-
SgK493.h ETLAQEMVHLFRSGQYLNQTSR-AEYORIP-
lias_TGFBR IPNRWQSCALRVMAKIMRECWTANG

